

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Weininger, Susan
Weininger, Arthur M

(ii) TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
SPECIFIC SEQUENCE COMPOSITION

(iii) NUMBER OF SEQUENCES: 118

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/860,844
(B) FILING DATE: 09-JUN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/353,476
(B) FILING DATE: 09-DEC-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Saliwanchik, David R.
(B) REGISTRATION NUMBER: 35,746
(C) REFERENCE/DOCKET NUMBER: GP-100C1

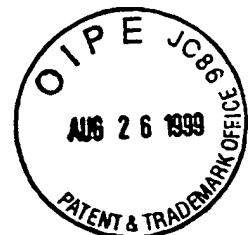
(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (352) 375-8100
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGGATTCC CCA

13

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

9/
(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGGACTTT CCC

13

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGGGGACTTT CCG

13

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGGGGACT TTCCA

15

(2) INFORMATION FOR SEQ ID NO:5:

- 51
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAAGGGACT TTCCG

15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGGTTTTTC CCC

13

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

9/ (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGGACTTT CCGCTGGGGA CTTTCCA

27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGGGACTTT CCGCTGGGGA CTTTCCG

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGGGGACT TTCCAGGGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

9/ (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTGGGGACT TTCCAGGGGA GGTGTG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTGGGGACT TTCCGGGGAG CGTGGC

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGGGGACT TTCCGGGGAG GCGCGG

26

(2) INFORMATION FOR SEQ ID NO:13:

- 91.
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCTGGGGACT TTCCAGAGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGGGGACT TTCCAGGGGA GCGTG

26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ca1 GCTGGGGACT TTCCAGGGAG GCGTGG

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTGGGGACT TTCCAGGGAG GCTGCC

26

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTCCAGGGA GCGTGGCCT GGGCGGGACT GGG

33

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

G/ (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGTGGCCTGG GCGGGACTGG GGAGTGGCGT CCC

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCT

45

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGCAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:21:

- 91
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATCAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGTG TGGCCT

46

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ca/ CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCAT

45

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGCGTG GCCT

44

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC GGGGAGGCGC GGCT

44

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

91 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGAGAGGCGT GGACT

45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGGAGGCG TGGACT

46

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTACAGGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGGGAG

46

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTACAGGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCTG CCT

43

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGG

48

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTCCAGGGA GGCCTGGCCT GGGCGGGACT GGGGAGTGGC GTCCC

45

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTACAAGGGA CTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGG

59

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTCCGCTGG GGACTTTCCA GGGAGGCGTG GCCTGGGCGG GACTGGGGAG TGGCGTCCC 59

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGGA 60

GTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TATCACCGCC AGTGGTATTT ATGTCAACAC CGCCAGAGAT AATTTATCAC CGCAGATGGT 60

T

61

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TATCACCGCA AGGGATAAAT ATCTAACACC GTGCGTGTTG ACTATTTTAC CTCTGGCGGT 60

GATA 64

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGCGT GGCCTGGGCG GGACTGGGGA 60

GTGGCGTCCC 70

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGG

37

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGGACTGGG GAGTGGCGTC CC

22

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTACAAGGGA CTTTCCGCTG GGGACTTTCC AGGGAGGTAT CACCGCCAGT GGTATTTATG

60

TCAACACCGC CAGAGATAAT TTATCACCGC AGATGGTTCT GCA

103

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAACCATCTG CGGTGATAAA TTATCTCTGG CGGTGTTGAC ATAAATACCA CTGGCGGTGA 60

TA 62

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCCAACCA TCTGCGGTGA TAAATTATCT CTGGCGGTGT TGACATAAAT ACCACTGGCG 60

GTGATACTGC A 71

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTATCACCGC CAGTGGTATT TATGTCAACA CCGCCAGAGA TAATTTATCA CCGCAGATGG 60

TTG 63

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GATCCGGGGG GATACCCCC G 21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGGACTGGG GAGTGGCGTC CCTATCACCG CAAGGGATAA ATATCTAACA CCGTGCGTGT 60

TGACTATTTT ACCTCTGGCG GTGATAGCAT G

91

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTAAGGGCGT AACCGAAATC GGTGAACCG AAACCGGTTA GTATAAAAGC AGA

53

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAAGGGAGT AACCGAAAAC GGTCGGGACC GAAAACGGTG TATATAAAAG ATGT

54

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTAGGGTGT AACCGAAAGC GGTTCACCG AAAACGGTGC ATATATAAAG CAAA

54

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCTTCAACCG AATTCGGTTG CATG

24

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTGCAACCG ATTCGGTTG CCTT

24

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TATGCAACCG AAATAGGTTG GGCA

24

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCCTAACCG TTTTCGGTTA CTTG

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGACTAACCG TTTTAGGTCA TATT

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GACGACTATC CAGCGACCAA GATCAGAGCC AGACACCGGA AACCCCTGCC AC

52

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GACGACACGG TATCCGCTAC TCAGCTTGTT AAACAGCTAC AGCACACCCC CTC

53

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GACGACGACC TGCAGACACC ACAGACACCG CCCAGCCCCT TACAAAGCTG TTCTGTGCAG 60

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CATACCAAAG CCGTCGCCTT GGGCACCGAA GAAACACAAC CACTAAGTTG TTGCACAGAG 60
ACTCAGTG 68

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TAATGTAATT GATTGTAATG ACTCTATGTG CAGTACCAGT ACCGTATTCC AGCACCGTGT 60
CCGTGGGCAC CGCAAAG 77

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAGACAACG ATAACCGACC ACCACAAGCA GCGGCCAAAC ACCCCGCCTT GGACAATAGA	60
ACAGCACGTA CTGCAACTAA	80

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATATGCAAT ACAATGCATT ATACAAACTG GACACATATA TATATTTGTG AAGAAGCATC	60
AGTAACTGTG GTAGAGGGTC AAGTTGACTA TTATGGTTTA TATTATGTTC ATGAAGGAAT	120
ACGAACATAT TTTGTGCAGT TTAAAGATGA TGCAGAAAAA TATAGTAAAA ATAAAGTATG	180
GGAAGTTCAT GCGGGTGGTC AGGTAATATT ATGTCCTACA TCTGTGTTTA GCAGCAACGA	240
AGTATCCTCT CCTGAAATTA TTAGGC	266

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AGGATGTATA AAAAAACATG GATATACAGT GGAAGTGCAG TTTGATGGAG ACATATGCTA	60
TTAGGCAGCA CTTGGCCAAC CACCCGCCG CGACC	95

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CATGTTTTTT TATACATCCA TATCACCGCC AGTGGTATTT ATGTCAACAC CGCCAGAGAT	60
AATTTATCAC CGCAGATGGT T	81

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	Ala	Asp	Asp	Asp	Pro	Tyr	Gly	Thr	Gly	Gln	Met	Phe	His	Leu	Asn	1	5	10	15
Thr	Ala	Leu	Thr	His	Ser	Ile	Phe	Asn	Ala	Glu	Leu	Tyr	Ser	Pro	Glu	20	25	30	
Ile	Pro	Leu	Ser	Thr	Asp	Gly	Pro	Tyr	Leu	Gln	Ile	Leu	Glu	Gln	Pro	35	40	45	
Lys	Gln	Arg	Gly	Phe	Arg	Phe	Arg	Tyr	Val	Cys	Glu	Gly	Pro	Ser	His	50	55	60	
Gly	Gly	Leu	Pro	Gly	Ala	Ser	Ser	Glu	Lys	Asn	Lys	Lys	Ser	Tyr	Pro	65	70	75	80
Gln	Val	Lys	Ile	Cys	Asn	Tyr	Val	Gly	Pro	Ala	Lys	Val	Ile	Val	Gln	85	90	95	
Leu	Val	Thr	Asn	Gly	Lys	Asn	Ile	His	Leu	His	Ala	His	Ser	Leu	Val	100	105	110	
Gly	Lys	His	Cys	Glu	Asp	Gly	Val	Cys	Thr	Val	Thr	Ala	Gly	Pro	Lys	115	120	125	
Asp	Met	Val	Val	Gly	Phe	Ala	Asn	Leu	Gly	Ile	Leu	His	Val	Thr	Lys	130	135	140	
Lys	Lys	Val	Phe	Glu	Thr	Leu	Glu	Ala	Arg	Met	Thr	Glu	Ala	Cys	Ile	145	150	155	160
Arg	Gly	Tyr	Asn	Pro	Gly	Leu	Leu	Val	His	Ser	Asp	Leu	Ala	Tyr	Leu	165	170	175	
Gln	Ala	Glu	Gly	Gly	Gly	Asp	Arg	Gln	Leu	Thr	Asp	Arg	Glu	Lys	Glu	180	185	190	
Ile	Ile	Arg	Gln	Ala	Ala	Val	Gln	Gln	Thr	Lys	Glu	Met	Asp	Leu	Ser	195	200	205	
Val	Val	Arg	Leu	Met	Phe	Thr	Ala	Phe	Leu	Pro	Asp	Ser	Thr	Gly	Ser	210	215	220	
Phe	Thr	Arg	Arg	Leu	Glu	Pro	Val	Val	Ser	Asp	Ala	Ile	Tyr	Asp	Ser	225	230	235	240
Lys	Ala	Pro	Asn	Ala	Ser	Asn	Leu	Lys	Ile	Val	Arg	Met	Asp	Arg	Thr	245	250	255	

(2) INFORMATION FOR SEQ ID NO:64:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met Phe His
1 5 10 15

Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val Phe Gln
20 25 30

Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu
35 40 45

Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
50 55 60

Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
65 70 75 80

Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
85 90 95

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Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
      100                      105                      110

Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala
      115                      120                      125

Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile Leu His
      130                      135                      140

Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
      145                      150                      155                      160

Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu
      165                      170                      175

Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly Asp Arg
      180                      185                      190

Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met
      195                      200                      205

Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
      210                      215                      220

Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
      225                      230                      235                      240

Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
      245                      250                      255

Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
      260                      265                      270

Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
      275                      280                      285

Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
      290                      295                      300

Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
      305                      310                      315                      320

Asp Ile Asn Ile Thr
      325

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(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Glu	Pro	Ala	Asp	Leu	Leu	Pro	Leu	Tyr	Leu	Gln	Pro	Glu	Trp	Gly	1	5	10	15
Glu	Gln	Glu	Pro	Gly	Gly	Ala	Thr	Pro	Phe	Val	Glu	Ile	Leu	Glu	Gln	20	25	30	
Pro	Lys	Gln	Arg	Gly	Met	Arg	Phe	Arg	Tyr	Lys	Cys	Glu	Gly	Arg	Ser	35	40	45	
Ala	Gly	Ser	Ile	Pro	Gly	Glu	His	Ser	Thr	Asp	Ser	Ala	Arg	Thr	His	50	55	60	
Pro	Thr	Ile	Arg	Val	Asn	His	Tyr	Arg	Gly	Pro	Gly	Arg	Val	Arg	Val	65	70	75	80
Ser	Leu	Val	Thr	Lys	Asp	Pro	Pro	His	Gly	Pro	His	Pro	His	Glu	Leu	85	90	95	
Val	Gly	Arg	His	Cys	Gln	His	Gly	Tyr	Tyr	Glu	Ala	Glu	Leu	Ser	Pro	100	105	110	
Asp	Arg	Ser	Ile	His	Ser	Phe	Gln	Asn	Leu	Gly	Ile	Gln	Cys	Val	Lys	115	120	125	
Lys	Arg	Glu	Leu	Glu	Ala	Ala	Val	Ala	Glu	Arg	Ile	Arg	Thr	Asn	Asn	130	135	140	
Asn	Pro	Phe	Asn	Val	Pro	Met	Glu	Glu	Arg	Gly	Ala	Glu	Tyr	Asp	Leu	145	150	155	160
Ser	Ala	Val	Arg	Leu	Cys	Phe	Gln	Val	Trp	Val	Asn	Gly	Pro	Gly	Gly	165	170	175	
Leu	Cys	Pro	Leu	Pro	Pro	Val	Leu	Ser	Gln	Pro	Ile	Tyr	Asp	Asn	Arg	180	185	190	
Ala	Pro	Ser	Thr	Ala	Glu	Leu	Arg	Ile	Leu	Pro	Gly	Asp	Arg	Asn	Ser	195	200	205	

Gly Ser Cys Gln Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val
 210 215 220
 Gln Lys Glu Asp Ile Glu Val Arg Phe Trp Ala Glu Gly Trp Glu Ala
 225 230 235 240
 Lys Gly Ser Phe Ala Ala Ala Asp Val His Arg Gln Val Ala Ile Val
 245 250 255
 Phe Arg Thr Pro Pro Phe Arg Glu Arg Ser Leu Arg
 260 265

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Asp Asp Leu Phe Pro Leu Ile Phe Pro Ser Glu Pro Ala Gln Ala
 1 5 10 15
 Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
 20 25 30
 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
 35 40 45
 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
 50 55 60
 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
 65 70 75 80
 Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
 85 90 95
 Asp Gly Tyr Tyr Glu Ala Asp Leu Cys Pro Asp Arg Ser Ile His Ser
 100 105 110

Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
 115 120 125
 Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe His Val Pro
 130 135 140
 Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
 145 150 155 160
 Phe Gln Val Thr Val Arg Asp Pro Ala Gly Arg Pro Leu Leu Leu Thr
 165 170 175
 Pro Val Leu Ser His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
 180 185 190
 Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
 195 200 205
 Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
 210 215 220
 Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
 225 230 235 240
 Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
 245 250 255
 Tyr Ala Asp Pro Ser Leu Gln
 260

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Asp Glu Leu Phe Pro Leu Ile Phe Pro Ala Glu Pro Ala Gln Ala
 1 5 10 15

Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
 20 25 30
 Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
 35 40 45
 Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
 50 55 60
 Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
 65 70 75 80
 Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
 85 90 95
 Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
 100 105 110
 Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
 115 120 125
 Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
 130 135 140
 Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
 145 150 155 160
 Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
 165 170 175
 Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
 180 185 190
 Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly
 195 200 205
 Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
 210 215 220
 Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
 225 230 235 240
 Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
 245 250 255
 Tyr Ala Asp Pro Ser Leu Gln
 260

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Phe	Pro	Asn	Gln	Asn	Asn	Gly	Ala	Ala	Pro	Gly	Gln	Gly	Pro	Ala	1	5	10	15
Val	Asp	Gly	Gln	Gln	Ser	Leu	Asn	Tyr	Asn	Gly	Leu	Pro	Ala	Gln	Gln	20	25	30	
Gln	Gln	Gln	Leu	Ala	Gln	Ser	Thr	Lys	Asn	Val	Arg	Lys	Lys	Pro	Tyr	35	40	45	
Val	Lys	Ile	Thr	Glu	Gln	Pro	Ala	Gly	Lys	Ala	Leu	Arg	Phe	Arg	Tyr	50	55	60	
Glu	Cys	Glu	Gly	Arg	Ser	Ala	Gly	Ser	Ile	Pro	Gly	Val	Asn	Ser	Thr	65	70	75	80
Pro	Glu	Asn	Lys	Thr	Tyr	Pro	Thr	Ile	Glu	Ile	Val	Gly	Tyr	Lys	Gly	85	90	95	
Arg	Ala	Val	Val	Val	Val	Ser	Cys	Val	Thr	Lys	Asp	Thr	Pro	Tyr	Arg	100	105	110	
Pro	His	Pro	His	Asn	Leu	Val	Gly	Lys	Glu	Gly	Cys	Lys	Lys	Gly	Val	115	120	125	
Cys	Thr	Leu	Glu	Ile	Asn	Ser	Glu	Thr	Met	Arg	Ala	Val	Phe	Ser	Asn	130	135	140	
Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Lys	Asp	Ile	Glu	Ala	Ala	Leu	Lys	145	150	155	160
Ala	Arg	Glu	Glu	Ile	Arg	Val	Asp	Pro	Phe	Lys	Thr	Gly	Phe	Ser	His	165	170	175	
Arg	Phe	Gln	Pro	Ser	Ser	Ile	Asp	Leu	Asn	Ser	Val	Arg	Leu	Cys	Phe	180	185	190	

Gln Val Phe Met Glu Ser Glu Gln Lys Gly Arg Phe Thr Ser Pro Leu
 195 200 205
 Pro Pro Val Val Ser Glu Pro Ile Phe Asp Lys Lys Ala Met Ser Asp
 210 215 220
 Leu Val Ile Cys Arg Leu Cys Ser Cys Ser Ala Thr Val Phe Gly Asn
 225 230 235 240
 Thr Gln Ile Ile Leu Leu Cys Glu Lys Val Ala Lys Glu Asp Ile Ser
 245 250 255
 Val Arg Phe Phe Glu Glu Lys Asn Gly Gln Ser Val Trp Glu Ala Phe
 260 265 270
 Gly Asp Phe Gln His Thr Asp Val His Lys Gln Thr Ala Ile Thr Phe
 275 280 285
 Lys Thr Pro Arg Tyr His Thr Leu Asp Ile Thr
 290 295

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Asp Phe Leu Thr Asn Leu Arg Phe Thr Glu Gly Ile Ser Glu Pro
 1 5 10 15
 Tyr Ile Glu Ile Phe Glu Gln Pro Arg Gln Arg Gly Thr Arg Phe Arg
 20 25 30
 Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly Glu His Ser
 35 40 45
 Thr Asp Asn Asn Lys Thr Phe Pro Ser Ile Gln Ile Leu Asn Tyr Phe
 50 55 60

Gly	Lys	Val	Lys	Ile	Arg	Thr	Thr	Leu	Val	Thr	Lys	Asn	Glu	Pro	Tyr	65	70	75	80
Lys	Pro	His	Pro	His	Asp	Leu	Val	Gly	Lys	Gly	Cys	Arg	Asp	Gly	Tyr	85	90	95	
Tyr	Glu	Ala	Glu	Phe	Gly	Pro	Glu	Arg	Gln	Val	Leu	Ser	Phe	Gln	Asn	100	105	110	
Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Lys	Asp	Leu	Lys	Glu	Ser	Ile	Ser	115	120	125	
Leu	Arg	Ile	Ser	Lys	Lys	Asn	Pro	Phe	Asn	Val	Pro	Glu	Glu	Gln	Leu	130	135	140	
His	Asn	Ile	Asp	Glu	Tyr	Asp	Leu	Asn	Val	Val	Arg	Leu	Cys	Phe	Gln	145	150	155	160
Ala	Phe	Leu	Pro	Asp	Glu	His	Gly	Asn	Tyr	Thr	Leu	Ala	Leu	Pro	Pro	165	170	175	
Leu	Ile	Ser	Asn	Pro	Ile	Tyr	Asp	Asn	Arg	Ala	Pro	Asn	Thr	Ala	Glu	180	185	190	
Leu	Arg	Ile	Cys	Arg	Val	Asn	Lys	Asn	Cys	Gly	Ser	Val	Lys	Gly	Gly	195	200	205	
Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Asp	Asp	Ile	Glu	210	215	220	
Val	Arg	Phe	Val	Leu	Gly	Asn	Trp	Glu	Ala	Lys	Gly	Ser	Phe	Ser	Gln	225	230	235	240
Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	Val	Phe	Arg	Thr	Pro	Pro	Phe	245	250	255	
Leu	Gly	Asp	Ile	Thr												260			

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Asp	Phe	Leu	Thr	Asn	Leu	Arg	Phe	Thr	Glu	Gly	Ile	Ser	Glu	Pro	1	5	10	15
Tyr	Ile	Glu	Ile	Phe	Glu	Gln	Pro	Arg	Gln	Arg	Gly	Met	Arg	Phe	Arg	20	25	30	
Tyr	Lys	Cys	Glu	Gly	Arg	Ser	Ala	Gly	Ser	Ile	Pro	Gly	Glu	His	Ser	35	40	45	
Thr	Asp	Asn	Asn	Lys	Thr	Phe	Pro	Ser	Ile	Gln	Ile	Leu	Asn	Tyr	Phe	50	55	60	
Gly	Lys	Val	Lys	Ile	Arg	Thr	Thr	Leu	Val	Thr	Lys	Asn	Glu	Pro	Tyr	65	70	75	80
Lys	Pro	His	Pro	His	Asp	Leu	Val	Gly	Lys	Gly	Cys	Arg	Asp	Gly	Tyr	85	90	95	
Tyr	Glu	Ala	Glu	Phe	Gly	Pro	Glu	Arg	Gln	Val	Leu	Ser	Phe	Gln	Asn	100	105	110	
Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Lys	Asp	Leu	Lys	Glu	Ser	Ile	Ser	115	120	125	
Leu	Arg	Ile	Ser	Lys	Lys	Ile	Asn	Pro	Phe	Asn	Val	Pro	Glu	Glu	Gln	130	135	140	
Leu	His	Asn	Ile	Asp	Glu	Tyr	Asp	Leu	Asn	Val	Val	Arg	Leu	Cys	Phe	145	150	155	160
Gln	Ala	Phe	Leu	Pro	Asp	Glu	His	Gly	Asn	Tyr	Thr	Leu	Ala	Leu	Pro	165	170	175	
Pro	Leu	Ile	Ser	Asn	Pro	Ile	Tyr	Asp	Asn	Arg	Ala	Pro	Asn	Thr	Ala	180	185	190	
Glu	Leu	Arg	Ile	Cys	Arg	Val	Asn	Lys	Asn	Cys	Gly	Ser	Val	Lys	Gly	195	200	205	
Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Asp	Asp	Ile	210	215	220	
Glu	Val	Arg	Phe	Val	Leu	Gly	Asn	Trp	Glu	Ala	Lys	Gly	Ser	Phe	Ser	225	230	235	240

Phe Leu Gly Asp Ile Thr
260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser Gln Gly Val Ile Gly Ile Phe Gly Asp Tyr Ala Lys Ala His Asp
20 25 30

Leu Ala Val Gly Glu Val Ser Lys Leu Val Lys Lys Ala Leu Ser Asn
35 40 45

Glu Tyr Pro Gln Leu Ser Phe Arg Tyr Arg Asp Ser Ile Lys Lys Thr
50 55 60

Glu Ile Asn Glu Ala Leu Lys Lys Ile Asp Pro Asp Leu Gly Gly Thr
65 70 75 80

Leu Phe Val Ser Asn Ser Ser Ile Lys Pro Asp Gly Gly Ile Val Glu
85 90 95

Val	Lys	Asp	Asp	Tyr	Gly	Glu	Trp	Arg	Val	Val	Leu	Val	Ala	Glu	Ala
			100					105					110		

Lys His Gln Gly Lys Asp Ile Ile Asn Ile Arg Asn Gly Leu Leu Val
115 120 125

Gly Lys Arg Gly Asp Gln Asp Leu Met Ala Ala Gly Asn Ala Ile Glu
130 135 140

Arg	Ser	His	Asn	Ile	Ser	Glu	Ile	Ala	Asn	Phe	Met	Leu	Ser	Glu	Ser	145	150	155	160
His	Phe	Pro	Tyr	Val	Leu	Phe	Leu	Glu	Gly	Ser	Asn	Phe	Leu	Thr	Glu	165	170	175	
Asn	Ile	Ser	Ile	Thr	Arg	Pro	Asp	Gly	Arg	Val	Val	Asn	Leu	Glu	Tyr	180	185	190	
Asn	Ser	Gly	Ser	Glu	Ser	His	Phe	Pro	Tyr	Val	Leu	Phe	Leu	Glu	Gly	195	200	205	
Ser	Asn	Phe	Leu	Thr	Glu	Asn	Ile	Ser	Ile	Thr	Arg	Pro	Asp	Gly	Arg	210	215	220	
Val	Val	Asn	Leu	Glu	Tyr	Asn	Ser	Gly	Ile	Leu	Asn	Arg	Leu	Asp	Arg	225	230	235	240
Leu	Thr	Ala	Ala	Asn	Tyr	Gly	Met	Pro	Ile	Asn	Ser	Asn	Leu	Cys	Ile	245	250	255	
Asn	Lys	Phe	Val	Asn	His	Lys	Asp	Lys	Ser	Ile	Met	Leu	Gln	Ala	Ala	260	265	270	
Ser	Ile	Tyr	Thr	Gln	Gly	Asp	Gly	Arg	Glu	Trp	Asp	Ser	Lys	Ile	Met	275	280	285	
Phe	Glu	Ile	Met	Phe	Asp	Ile	Ser	Thr	Thr	Ser	Leu	Arg	Val	Leu	Gly	290	295	300	
Arg	Asp	Leu	Phe	Glu	Gln	Leu	Thr	Ser	Lys							305	310		

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Cys Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Lys
 1 5 10 15

Thr

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Asp Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly Cys
 1 5 10 15

Gly Lys Val Tyr Gly Lys Thr Ser His Leu Arg Ala His Leu Arg Trp
 20 25 30

His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly Lys
 35 40 45

Arg Phe Thr Arg Ser Asp Glu Leu Gln Arg His Lys Arg Thr His Thr
 50 55 60

Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met Arg
 65 70 75 80

Ser Asp His Leu Ser Lys His Ile Lys Thr His Gln Asn Lys Lys Gly
 85 90 95

Gly Pro Gly Val Ala Leu Ser Val Gly Thr Leu Pro Leu Asp Ser Gly
 100 105 110

Ala Gly Ser Glu Gly Ser Gly Thr Ala Thr Pro Ser Ala Leu Ile Thr
 115 120 125

Thr Asn Met Val Ala Met Glu Ala Ile Cys Pro Glu Gly Ile Ala Arg
 130 135 140

Leu Ala Asn Ser Gly Ile Asn Val Met Gln Val Ala Asp Leu Gln Ser
 145 150 155 160

Ile Asn Ile Ser Gly Asn Gly Phe
 165

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Gly Ile Val Pro Gln Leu Gln Asn Ile Val Ser Thr Val Asn Leu
 1 5 10 15

Gly Cys Lys Leu Asp Leu Lys Thr Ile Ala Leu Arg Ala Arg Asn Ala
 20 25 30

Glu Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu
 35 40 45

Pro Arg Thr Thr Ala Leu Ile Phe Ser Ser Gly Lys Met Val Cys Thr
 50 55 60

Gly Ala Lys Ser Glu Glu Gln Ser Arg Leu Ala Ala Arg Lys Tyr Ala
 65 70 75 80

Arg Val Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Leu Asp Phe Lys
 85 90 95

Ile Gln Asn Met Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu
 100 105 110

Glu Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu
 115 120 125

Leu Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu
 130 135 140

Leu Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg
 145 150 155 160

Ala Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly
 165 170 175

Phe Arg Lys Thr Thr
 180

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Cys Phe Ala Leu Ile Ser Gly Thr Ala Asn Gln Val Lys Cys Tyr
 1 5 10 15

Arg Phe Arg Val Lys Lys Asn His Arg His Arg Tyr Glu Asn Cys Thr
 20 25 30

Thr Thr Trp Phe Thr Val Ala Asp Asn Gly Ala Glu Arg Gln Gly Gln
 35 40 45

Ala Gln Ile Leu Ile Thr Phe Gly Ser Pro Ser Gln Arg Gln Asp Phe
 50 55 60

Leu Lys His Val Pro Leu Pro Pro Gly Met Asn Ile Ser Gly Phe Thr
 65 70 75 80

Ala Ser Leu Asp Phe
 85

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Cys	Pro	Cys	Leu	Leu	Ile	Gly	Thr	Ser	Gly	Asn	Gly	Asn	Gln	Val	Lys
1			5						10					15	

Cys	Tyr	Ser	Phe	Arg	Val	Lys	Arg	Trp	His	Asp	Arg	Asp	Lys	Tyr	His
			20					25					30		

His	Thr	Thr	Thr	Trp	Trp	Ala	Val	Gly	Gly	Gln	Gly	Ser	Glu	Arg	Pro
		35					40					45			

Gly	Asp	Ala	Thr	Val	Ile	Val	Thr	Phe	Lys	Asp	Gln	Ser	Gln	Arg	Ser
	50					55					60				

His	Phe	Leu	Gln	Gln	Val	Pro	Leu	Pro	Pro	Gly	Met	Ser	Ala	His	Gly
65					70					75					80

Val	Thr	Met	Thr	Val	Asp	Phe
				85		

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Pro	Pro	Val	Ile	Cys	Leu	Lys	Gly	Gly	His	Asn	Gln	Leu	Lys	Cys	Leu
1				5					10					15	

Arg Tyr Arg Leu Lys Ser Lys His Ser Ser Leu Phe Asp Cys Ile Ser
 20 25 30

Thr Thr Trp Ser Trp Val Asp Thr Thr Ser Thr Cys Arg Leu Gly Ser
 35 40 45

Gly Arg Met Leu Ile Lys Phe Ala Asp Ser Glu Gln Arg Asp Lys Phe
 50 55 60

Leu Ser Arg Val Pro Leu Pro Ser Thr Thr Gln Val Phe Leu Gly Asn
 65 70 75 80

Phe Tyr Gly Leu

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Pro Val Ile Leu Val Arg Gly Gly Ala Asn Thr Leu Lys Cys Phe
 1 5 10 15

Arg Asn Arg Ala Arg Val Arg Tyr Arg Gly Leu Phe Lys Tyr Phe Ser
 20 25 30

Thr Thr Trp Ser Trp Val Ala Gly Asp Ser Thr Glu Arg Leu Gly Arg
 35 40 45

Ser Arg Met Leu Ile Leu Phe Thr Ser Ala Cys Gln Arg Glu Lys Pro
 50 55 60

Asp Glu Thr Val Lys Tyr Pro Lys Gly Val Asp Thr Ser Tyr Gly Asn
 65 70 75 80

Leu Asp Ser Leu

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Pro	Pro	Val	Val	Cys	Val	Lys	Gly	Gly	Ala	Asn	Gln	Leu	Lys	Cys	Leu
1				5					10					15	
Arg	Tyr	Arg	Leu	Lys	Ala	Ser	Thr	Gln	Val	Asp	Phe	Asp	Ser	Ile	Ser
			20					25					30		
Thr	Thr	Trp	His	Trp	Thr	Asp	Arg	Lys	Asn	Thr	Glu	Arg	Ile	Gly	Ser
		35					40					45			
Ala	Arg	Met	Leu	Val	Lys	Phe	Ile	Asp	Glu	Ala	Gln	Arg	Glu	Lys	Phe
	50					55					60				
Leu	Glu	Arg	Val	Ala	Leu	Pro	Arg	Ser	Val	Ser	Val	Phe	Leu	Gly	Gln
65					70					75				80	
Phe	Asn	Gly	Ser												

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Thr	Pro	Ile	Val	Gln	Leu	Gln	Gly	Asp	Ser	Asn	Cys	Leu	Lys	Cys	Phe
1				5					10					15	
Arg	Tyr	Arg	Leu	Asn	Asp	Lys	Tyr	Lys	His	Leu	Phe	Glu	Leu	Ala	Ser
			20					25					30		
Ser	Thr	Trp	His	Trp	Ala	Ser	Pro	Glu	Ala	Pro	His	Lys	Asn	Ala	Ile
		35					40					45			
Val	Thr	Leu	Thr	Tyr	Ser	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asn
	50					55					60				
Ser	Val	Lys	Ile	Pro	Pro	Thr	Ile	Arg	His	Lys	Val	Gly	Phe	Met	Ser
65					70					75					80
Leu	His	Leu	Leu												

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Thr	Pro	Ile	Val	Gln	Phe	Gln	Gly	Glu	Ser	Asn	Cys	Leu	Lys	Cys	Phe
1				5					10					15	
Arg	Tyr	Arg	Leu	Asn	Arg	Asp	His	Arg	His	Leu	Phe	Asp	Leu	Ile	Ser
			20					25					30		
Ser	Thr	Trp	His	Trp	Ala	Ser	Ser	Lys	Ala	Pro	His	Lys	His	Ala	Ile
		35					40					45			
Val	Thr	Val	Thr	Tyr	Asp	Ser	Glu	Glu	Gln	Arg	Gln	Gln	Phe	Leu	Asp
	50					55					60				

Val Val Lys Ile Pro Pro Thr Ile Ser His Lys Leu Gly Phe Met Ser
65 70 75 80

Leu His Leu Leu

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Pro Ile Ile His Leu Lys Gly Asp Arg Asn Ser Leu Lys Cys Leu
1 5 10 15

Arg Tyr Arg Leu Arg Lys His Ser Asp His Tyr Arg Asp Ile Ser Ser
20 25 30

Thr Trp His Trp Thr Gly Ala Gly Asn Glu Lys Thr Gly Ile Leu Thr
35 40 45

Val Thr Tyr His Ser Glu Thr Gln Arg Thr Lys Phe Leu Asn Thr Val
50 55 60

Ala Ile Pro Asp Ser Val Gln Ile Leu Val Gly Tyr Asn Thr Met Tyr
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr	Pro	Ile	Val	His	Leu	Lys	Gly	Asp	Ala	Asn	Thr	Leu	Lys	Cys	Leu
1				5				10						15	
Arg	Tyr	Arg	Phe	Lys	Lys	His	Cys	Thr	Leu	Tyr	Thr	Ala	Val	Ser	Ser
			20					25					30		
Thr	Trp	His	Trp	Thr	Gly	His	Asn	Tyr	Lys	His	Lys	Ser	Ala	Ile	Val
		35					40					45			
Thr	Leu	Thr	Tyr	Asp	Ser	Glu	Trp	Gln	Arg	Asp	Gln	Phe	Leu	Ser	Gln
	50					55					60				
Val	Lys	Ile	Pro	Lys	Thr	Ile	Thr	Val	Ser	Thr	Gly	Phe	Met	Ser	Ile
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ala	Pro	Ile	Val	His	Leu	Lys	Gly	Glu	Ser	Asn	Ser	Leu	Lys	Cys	Leu
1				5				10						15	
Arg	Tyr	Arg	Leu	Lys	Pro	Tyr	Asn	Glu	Leu	Tyr	Ser	Ser	Met	Ser	Ser
			20					25					30		
Thr	Trp	His	Trp	Thr	Ser	Asp	Asn	Lys	Asn	Ser	Lys	Asn	Gly	Ile	Val
		35					40					45			
Thr	Val	Thr	Phe	Val	Thr	Gly	Gln	Gln	Gln	Gln	Met	Phe	Leu	Gly	Thr
	50					55					60				

Val Lys Ile Pro Pro Thr Val Gln Ile Ser Thr Gly Phe Met Thr Leu
 65 70 75 80

Val

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
 1 5 10 15

Glu Asn Tyr Cys Asn
 20

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:87:

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Gly Ile Val Glu Gln Cys Cys Ala Ser Val Cys Ser Leu Tyr Gln Leu
1 5 10 15
Glu Asn Tyr Cys Asn
20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Gln	Leu	Tyr	Ser	Ala	Leu	Ala	Asn	Lys	Cys	Cys	His	Val	Gly	Cys	Ile
1				5					10					15	
Lys Arg Ser Leu Ala Arg Phe Cys															
20															

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Asp	Ser	Trp	Met	Glu	Glu	Val	Ile	Lys	Ile	Cys	Gly	Arg	Glu	Leu	Val
1				5					10					15	
Arg	Ala	Gln	Ile	Ala	Ile	Cys	Gly	Met	Ser	Thr	Trp	Ser	Lys	Arg	Ser
			20					25					30		
Leu															

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu	Glu	Lys	Met	Gly	Thr	Ala	Lys	Lys	Cys	Cys	Ala	Ile	Gly	Cys	Ser
1				5					10					15	
Thr	Glu	Asp	Phe	Arg	Met	Val	Cys								
								20							

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Arg	Pro	Asn	Trp	Glu	Glu	Arg	Ser	Arg	Leu	Cys	Gly	Arg	Asp	Leu	Ile	
1				5					10					15		
Arg	Ala	Phe	Ile	Tyr	Leu	Cys	Gly	Gly	Thr	Arg	Trp	Thr	Arg	Leu	Pro	
				20					25					30		
Asn	Phe	Gly	Asn	Tyr	Pro	Ile	Met									
							35				40					

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ser Gly Ile Val Pro Thr Leu Gln Asn Ile Val Ser Thr Val Asn Leu
 1 5 10 15

Asp Cys Lys Leu Asp Leu Lys Ala Ile Ala Leu Gln Ala Arg Asn Ala
 20 25 30

Glu Tyr Asn Pro Lys Arg Phe Ala Ala Val Ile Met Arg Ile Arg Glu
 35 40 45

Pro Lys Thr Thr Ala Leu Ile Phe Ala Ser Gly Lys Met Val Cys Thr
 50 55 60

Gly Ala Lys Ser Glu Asp Phe Ser Lys Met Ala Ala Arg Lys Tyr Ala
 65 70 75 80

Arg Ile Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Lys Asp Phe Lys
 85 90 95

Ile Gln Asn Ile Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu
 100 105 110

Glu Gly Leu Ala Tyr Ser His Ala Ala Phe Ser Ser Tyr Glu Pro Glu
 115 120 125

Leu Phe Pro Gly Leu Ile Tyr Arg Met Lys Val Pro Lys Ile Val Leu
 130 135 140

Leu Ile Phe Val Ser Gly Lys Ile Val Ile Thr Gly Ala Lys Met Arg
 145 150 155 160

Asp Glu Thr Tyr Lys Ala Phe Glu Asn Ile Tyr Pro Val Leu Ser Glu
 165 170 175

Phe Arg Lys Ile Gln Gln
180

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asn	Ser	Asn	Ser	Thr	Pro	Ile	Val	His	Leu	Lys	Gly	Asp	Ala	Asn	Thr
1				5					10					15	
Leu	Lys	Cys	Leu	Arg	Tyr	Arg	Phe	Lys	Lys	His	Cys	Thr	Leu	Tyr	Thr
			20					25					30		
Ala	Val	Ser	Ser	Thr	Trp	His	Trp	Thr	Gly	His	Asn	Val	Lys	His	Lys
		35					40					45			
Ser	Ala	Ile	Val	Thr	Leu	Thr	Tyr	Asp	Ser	Glu	Trp	Gln	Arg	Asp	Gln
	50					55				60					
Phe	Leu	Ser	Gln	Val	Lys	Ile	Pro	Lys	Thr	Ile	Thr	Val	Ser	Thr	Gly
65					70					75					80
Phe Met Ser Ile															

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Asn Ser Asn Thr Thr Pro Ile Val His Leu Lys Gly Asp Ala Asn Thr
1           5           10           15
Leu Lys Cys Leu Arg Tyr Arg Phe Lys Lys His Cys Thr Leu Tyr Thr
          20           25           30
Ala Val Ser Ser Thr Trp His Trp Thr Gly His Asn Val Lys His Lys
          35           40           45
Ser Ala Ile Val Thr Leu Thr Tyr Asp Ser Glu Trp Gln Arg Asp Gln
          50           55           60
Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
65           70           75           80
Phe Met Ser Ile

```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Ser Gly Asn Thr Thr Pro Ile Ile His Leu Lys Gly Asp Arg Asn Ser
1           5           10           15
Leu Lys Cys Leu Arg Tyr Arg Leu Arg Lys His Ser Asp His Tyr Arg
          20           25           30
Asp Ile Ser Ser Thr Trp His Trp Thr Gly Ala Gly Asn Glu Lys Thr
          35           40           45

```

Gly Ile Leu Thr Val Thr Tyr His Ser Glu Thr Gln Arg Thr Lys Phe
 50 55 60

Leu Asn Thr Val Ala Ile Pro Asp Ser Val Gln Ile Leu Val Gly Tyr
 65 70 75 80

Met Thr Met

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Gly Asn Thr Ala Pro Ile Val His Leu Lys Gly Glu Ser Asn Ser
 1 5 10 15

Leu Lys Cys Leu Arg Tyr Arg Leu Lys Pro Tyr Lys Glu Leu Tyr Ser
 20 25 30

Ser Met Ser Ser Thr Trp His Trp Thr Ser Asp Asn Lys Asn Ser Lys
 35 40 45

Asn Gly Ile Val Thr Val Thr Phe Val Thr Glu Gln Gln Gln Gln Met
 50 55 60

Phe Leu Gly Thr Val Lys Ile Pro Pro Thr Val Gln Ile Ser Thr Gly
 65 70 75 80

Phe Met Thr Leu

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser	Gly	Asn	Thr	Ser	Cys	Phe	Ala	Leu	Ile	Ser	Gly	Thr	Ala	Asn	Gln
1				5					10					15	
Val	Lys	Cys	Tyr	Arg	Phe	Arg	Val	Lys	Lys	Asn	His	Arg	His	Arg	Tyr
			20					25					30		
Glu	Asn	Cys	Thr	Thr	Thr	Trp	Phe	Thr	Val	Ala	Asp	Asn	Gly	Ala	Glu
		35					40					45			
Arg	Gln	Gly	Gln	Ala	Gln	Ile	Leu	Ile	Thr	Phe	Gly	Ser	Pro	Ser	Gln
	50					55					60				
Arg	Gln	Asp	Phe	Leu	Lys	His	Val	Pro	Leu	Pro	Pro	Gly	Met	Asn	Ile
65					70				75					80	
Ser	Gly	Phe	Thr	Ala	Ser	Leu	Asp	Phe							
						85									

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Ser	Asn	Lys	Lys	Thr	Thr	Ala
1				5		

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asn Ser Asn Thr
1

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Gly Asn Thr
1

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Ser Ser Gly Ser Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Cys Tyr Pro Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Met Glu Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1           5           10           15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
          20           25           30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
          35           40           45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
          50           55           60

Thr Ala
65

```

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1           5           10           15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
          20           25           30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
          35           40           45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
          50           55           60

Thr Ala
65

```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1           5           10           15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
          20           25           30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
          35           40           45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
          50           55           60

Thr Ala
65
  
```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

Ser Thr Lys Lys Lys Pro Leu Thr Gln Glu Gln Leu Glu Asp Ala Arg
1           5           10           15
  
```

```

Arg Leu Lys Ala Ile Tyr Glu Lys Lys Lys Asn Glu Leu Gly Leu Ser
      20              25              30

Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val Gly
      35              40              45

Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala Leu
      50              55              60

Leu Ala Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser Ile
      65              70              75              80

Ala Arg Glu Ile Tyr Glu Met Tyr Glu Ala Val Ser Met Glu Pro Ser
      85              90              95

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Ser Thr Lys Lys Lys Pro Leu Thr Gln Glu Gln Leu Glu Asp Ala Arg
1              5              10              15

Arg Leu Lys Ala Ile Tyr Glu Lys Lys Lys Asn Glu Leu Gly Leu Ser
      20              25              30

Gln Glu Ser Val Ala Asp Lys Met Gly Met Gly Gln Ser Gly Val Gly
      35              40              45

Ala Leu Phe Asn Gly Ile Asn Ala Leu Asn Ala Tyr Asn Ala Ala Leu
      50              55              60

Leu Ala Lys Ile Leu Lys Val Ser Val Glu Glu Phe Ser Pro Ser Ile
      65              70              75              80

Ala Arg Glu Ile Tyr Glu Met Cys Glu Ala Val Ser Met Glu Pro Ser
      85              90              95

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gly	Ile	Val	Glu	Gln	Cys	Cys	Thr	Ser	Ile	Cys	Ser	Leu	Tyr	Gln	Leu	1	5	10	15
Glu	Asn	Tyr	Cys	Asn	Met	Ser	Met	Glu	Gln	Arg	Ile	Thr	Leu	Lys	Asp	20	25	30	
Tyr	Ala	Met	Arg	Phe	Gly	Gln	Thr	Lys	Thr	Ala	Lys	Asp	Leu	Gly	Val	35	40	45	
Tyr	Gln	Ser	Ala	Ile	Asn	Lys	Ala	Ile	His	Ala	Gly	Arg	Lys	Ile	Phe	50	55	60	
Leu	Thr	Ile	Asn	Ala	Asp	Gly	Ser	Val	Tyr	Ala	Glu	Glu	Val	Lys	Pro	65	70	75	80
Phe	Pro	Ser	Asn	Lys	Lys	Thr	Thr	Ala	Ser	Asn	Lys	Lys	Thr	Thr	Ala	85	90	95	
Asn	Ser	Asn	Thr	Thr	Pro	Ile	Val	His	Leu	Lys	Gly	Asp	Ala	Asn	Thr	100	105	110	
Leu	Lys	Cys	Leu	Arg	Tyr	Arg	Phe	Lys	Lys	His	Cys	Thr	Leu	Tyr	Thr	115	120	125	
Ala	Val	Ser	Ser	Thr	Trp	His	Trp	Thr	Gly	His	Asn	Val	Lys	His	Lys	130	135	140	
Ser	Ala	Ile	Val	Thr	Leu	Thr	Tyr	Asp	Ser	Glu	Trp	Gln	Arg	Asp	Gln	145	150	155	160

Phe Leu Ser Gln Val Lys Ile Pro Lys Thr Ile Thr Val Ser Thr Gly
 165 170 175

Phe Met Ser Ile
 180

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
 1 5 10 15

Glu Asn Tyr Cys Asn Met Ser Met Glu Gln Arg Ile Thr Leu Lys Asp
 20 25 30

Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp Leu Gly Val
 35 40 45

Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg Lys Ile Phe
 50 55 60

Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu Val Lys Pro
 65 70 75 80

Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys Thr Thr Ala
 85 90 95

Cys Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg Lys
 100 105 110

Thr

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Ser	His	Leu	Val	Glu	Ala	Leu	Tyr	1	5	10	15
Leu	Val	Cys	Gly	Glu	Arg	Gly	Phe	Phe	Tyr	Thr	Pro	Lys	Thr	Met	Ser	20	25	30	
Met	Glu	Gln	Glu	Ile	Thr	Leu	Lys	Asp	Tyr	Ala	Met	Arg	Phe	Gly	Gln	35	40	45	
Thr	Lys	Thr	Ala	Lys	Asp	Leu	Gly	Val	Tyr	Gln	Ser	Ala	Ile	Asn	Lys	50	55	60	
Ala	Ile	His	Ala	Gly	Arg	Lys	Ile	Phe	Leu	Thr	Ile	Asn	Ala	Asp	Gly	65	70	75	80
Ser	Val	Tyr	Ala	Glu	Glu	Val	Lys	Pro	Phe	Pro	Ser	Asn	Lys	Lys	Thr	85	90	95	
Thr	Ala	Ser	Asn	Lys	Lys	Thr	Thr	Ala	Ser	Ser	Gly	Ser	Ser	Gly	Ser	100	105	110	
Gly	Ile	Val	Pro	Gln	Leu	Gln	Asn	Ile	Val	Ser	Thr	Val	Asn	Leu	Gly	115	120	125	
Cys	Lys	Leu	Asp	Leu	Lys	Thr	Ile	Ala	Leu	Arg	Ala	Arg	Asn	Ala	Glu	130	135	140	
Tyr	Asn	Pro	Lys	Arg	Phe	Ala	Ala	Val	Ile	Met	Arg	Ile	Arg	Glu	Pro	145	150	155	160
Arg	Thr	Thr	Ala	Leu	Ile	Phe	Ser	Ser	Gly	Lys	Met	Val	Cys	Thr	Gly	165	170	175	
Ala	Lys	Ser	Glu	Glu	Gln	Ser	Arg	Leu	Ala	Ala	Arg	Lys	Tyr	Ala	Arg	180	185	190	

Val Val Gln Lys Leu Gly Phe Pro Ala Lys Phe Leu Asp Phe Lys Ile
 195 200 205

Gln Asn Met Val Gly Ser Cys Asp Val Lys Phe Pro Ile Arg Leu Glu
 210 215 220

Gly Leu Val Leu Thr His Gln Gln Phe Ser Ser Tyr Glu Pro Glu Leu
 225 230 235 240

Phe Pro Gly Leu Ile Tyr Arg Met Ile Lys Pro Arg Ile Val Leu Leu
 245 250 255

Ile Phe Val Ser Gly Lys Val Val Leu Thr Gly Ala Lys Val Arg Ala
 260 265 270

Glu Ile Tyr Glu Ala Phe Glu Asn Ile Tyr Pro Ile Leu Lys Gly Phe
 275 280 285

Arg Lys Thr Thr
 290

91 (2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
 1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Met Ser
 20 25 30

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
 35 40 45

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 50 55 60

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 65 70 75 80
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 85 90 95
 Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys
 100 105 110
 Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr
 115 120 125
 Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe
 130 135 140
 Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu
 145 150 155 160
 Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys
 165 170 175
 Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His
 180 185 190
 Ile Lys Thr His Gln Asn Lys Lys Gly Gly Pro Gly Val Ala Leu Ser
 195 200 205
 Val Gly Thr Leu Pro Leu Asp Ser Gly Ala Gly Ser Glu Gly Ser Gly
 210 215 220
 Thr Ala Thr Pro Ser Ala Leu Ile Thr Thr Asn Met Val Ala Met Glu
 225 230 235 240
 Ala Ile Cys Pro Glu Gly Ile Ala Arg Leu Ala Asn Ser Gly Ile Asn
 245 250 255
 Val Met Gln Val Ala Asp Leu Gln Ser Ile Asn Ile Ser Gly Asn Gly
 260 265 270
 Phe

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Ile
 1 5 10 15
 Lys Arg Ser Leu Ala Arg Phe Cys Met Ser Met Arg Gln Arg Ile Thr
 20 25 30
 Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln Thr Lys Thr Ala Lys Asp
 35 40 45
 Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys Ala Ile His Ala Gly Arg
 50 55 60
 Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly Ser Val Tyr Ala Glu Glu
 65 70 75 80
 Val Lys Pro Phe Pro Ser Asn Lys Lys Thr Thr Ala Ser Asn Lys Lys
 85 90 95
 Thr Thr Ala Met Ala Asp Asp Asp Pro Tyr Gly Thr Gly Gln Met Phe
 100 105 110
 His Leu Asn Thr Ala Leu Thr His Ser Ile Phe Asn Ala Glu Leu Tyr
 115 120 125
 Ser Pro Glu Ile Pro Leu Ser Thr Asp Gly Pro Tyr Leu Gln Ile Leu
 130 135 140
 Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
 145 150 155 160
 Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
 165 170 175
 Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
 180 185 190
 Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
 195 200 205
 Ser Leu Val Gly Lys His Cys Glu Asp Gly Val Cys Thr Val Thr Ala
 210 215 220

Gly Pro Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His
 225 230 235 240
 Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
 245 250 255
 Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Ser Asp Leu
 260 265 270
 Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Thr Asp Arg
 275 280 285
 Glu Lys Glu Ile Ile Arg Gln Ala Ala Val Gln Gln Thr Lys Glu Met
 290 295 300
 Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
 305 310 315 320
 Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
 325 330 335
 Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
 340 345 350
 Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
 355 360 365
 Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
 370 375 380
 Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
 385 390 395 400
 Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
 405 410 415
 Asp Val Asn Ile Thr
 420

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
20 25 30

Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
35 40 45

Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
50 55 60

Thr Ala Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met
65 70 75 80

Phe His Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val
85 90 95

Phe Gln Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln
100 105 110

Ile Leu Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys
115 120 125

Glu Gly Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn
130 135 140

Lys Lys Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala
145 150 155 160

Lys Val Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His
165 170 175

Ala His Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val
180 185 190

Thr Ala Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile
195 200 205

Leu His Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met
210 215 220

Thr Glu Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro
225 230 235 240

Asp Leu Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly
 245 250 255
 Asp Arg Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys
 260 265 270
 Glu Met Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro
 275 280 285
 Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp
 290 295 300
 Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val
 305 310 315 320
 Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr
 325 330 335
 Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr
 340 345 350
 Glu Glu Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser
 355 360 365
 Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys
 370 375 380
 Tyr Lys Asp Ile Asn Ile Thr
 385 390

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Glu Gln Glu Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
 1 5 10 15

Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 20 25 30
 Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 35 40 45
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60
 Thr Ala Met Ala Glu Asp Asp Pro Tyr Leu Gly Arg Pro Glu Gln Met
 65 70 75 80
 Phe His Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val
 85 90 95
 Phe Gln Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln
 100 105 110
 Ile Leu Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys
 115 120 125
 Glu Gly Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn
 130 135 140
 Lys Lys Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala
 145 150 155 160
 Lys Val Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His
 165 170 175
 Ala His Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val
 180 185 190
 Thr Ala Gly Pro Glu Asp Cys Val His Gly Phe Ala Asn Leu Gly Ile
 195 200 205
 Leu His Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met
 210 215 220
 Thr Glu Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro
 225 230 235 240
 Asp Leu Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly
 245 250 255
 Asp Arg Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys
 260 265 270
 Glu Met Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro
 275 280 285

G1

Asp Ser Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp
 290 295 300
 Ala Ile Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val
 305 310 315 320
 Arg Met Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr
 325 330 335
 Leu Leu Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr
 340 345 350
 Glu Glu Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser
 355 360 365
 Pro Thr Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys
 370 375 380
 Tyr Lys Asp Ile Asn Ile Thr
 385 390

91 (2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Arg Gln Arg Ile Thr Leu Lys Asp Tyr Ala Met Arg Phe Gly Gln
 1 5 10 15
 Thr Lys Thr Ala Lys Asp Leu Gly Val Tyr Gln Ser Ala Ile Asn Lys
 20 25 30
 Ala Ile His Ala Gly Arg Lys Ile Phe Leu Thr Ile Asn Ala Asp Gly
 35 40 45
 Ser Val Tyr Ala Glu Glu Val Lys Pro Phe Pro Ser Asn Lys Lys Thr
 50 55 60

Thr Ala Ser Asn Lys Lys Thr Thr Ala Gly Asp Pro Gly Lys Lys Lys
 65 70 75 80
 Gln His Ile Cys His Ile Gln Gly Cys Gly Lys Val Tyr Gly Lys Thr
 85 90 95
 Ser His Leu Arg Ala His Leu Arg Trp His Thr Gly Glu Arg Pro Phe
 100 105 110
 Met Cys Thr Trp Ser Tyr Cys Gly Lys Arg Phe Thr Arg Ser Asp Glu
 115 120 125
 Leu Gln Arg His Lys Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys
 130 135 140
 Pro Glu Cys Pro Lys Arg Phe Met Arg Ser Asp His Leu Ser Lys His
 145 150 155 160
 Ile Lys Thr His Gln Asn Lys Lys Gly Gly Pro Gly Val Ala Leu Ser
 165 170 175
 Val Gly Thr Leu Pro Leu Asp Ser Gly Ala Gly Ser Glu Gly Ser Gly
 180 185 190
 Thr Ala Thr Pro Ser Ala Leu Ile Thr Thr Asn Met Val Ala Met Glu
 195 200 205
 Ala Ile Cys Pro Glu Gly Ile Ala Arg Leu Ala Asn Ser Gly Ile Asn
 210 215 220
 Val Met Gln Val Ala Asp Leu Gln Ser Ile Asn Ile Ser Gly Asn Gly
 225 230 235 240
 Phe

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGGAMTNYCC

10

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala His Gln Asn Ser Gln Thr
50 55 60

His Gln Ala Ser Leu Ser Lys Gln
65 70